

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/588, 140  
Source: IFW0  
Date Processed by STIC: 08/10/2006

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 08/10/2006

PATENT APPLICATION: US/10/588,140

TIME: 10:59:47

Input Set : A:\44352-0010-00-US sequence listing(pct 05 234).txt

Output Set: N:\CRF4\08102006\J588140.raw

```

3 <110> APPLICANT: Lifenza Co., Ltd.
5 <120> TITLE OF INVENTION: PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH, MUTAN,
6     INULIN AND LEVANN, GENE ENCODING THE SAME, CELL EXPRESSING THE
7     SAME, AND PRODUCTION METHOD THEREOF
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/588,140
C--> 9 <141> CURRENT FILING DATE: 2006-07-31
W--> 0 <130> FILE REFERENCE:
      9 <150> PRIOR APPLICATION NUMBER: KR2004-0006185
10 <151> PRIOR FILING DATE: 2004-01-30
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: KopatentIn 1.71
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 608
18 <212> TYPE: PRT
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: S. cerevisiae/pYES2-LSD1
25 <400> SEQUENCE: 1
26 Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
27   1           5           10           15
29 Thr Arg Ile Val Leu Val Asn Ile Leu Ala Thr Leu Val Leu Gly
30           20           25           30
32 Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
33           35           40           45
35 Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
36           50           55           60
38 Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser
39   65           70           75           80
41 Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
42           85           90           95
44 Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
45           100          105          110
47 Ser Asn Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro
48           115          120          125
50 Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp
51           130          135          140
53 Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro
54   145          150          155          160
56 Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg
57           165          170          175
59 Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg
60           180          185          190
62 Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp

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```

63          195          200          205
65 Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro
66          210          215          220
68 Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met
69 225          230          235          240
71 Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro
72          245          250          255
74 Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro
75          260          265          270
77 Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu
78          275          280          285
80 Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu
81          290          295          300
83 Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln
84 305          310          315          320
86 Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val
87          325          330          335
89 Tyr Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly
90          340          345          350
92 Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr
93          355          360          365
95 Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met
96          370          375          380
98 Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys
99 385          390          395          400
101 Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu
102          405          410          415
104 Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
105          420          425          430
107 Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
108          435          440          445
110 Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
111          450          455          460
113 Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
114 465          470          475          480
116 Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
117          485          490          495
119 Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
120          500          505          510
122 Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
123          515          520          525
125 Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
126          530          535          540
128 Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
129 545          550          555          560
131 Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
132          565          570          575
134 Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
135          580          585          590

```

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```

137 Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
138      595      600      605
143 <210> SEQ ID NO: 2
144 <211> LENGTH: 2052
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: S. cerevisiae/pYLSd1
152 <400> SEQUENCE: 2
153 tgggtgtgtc cttgtctctg ccaacgttgt tgattgtttt catgacatta atctacgtgc      60
155 cttcaatatt tacaatggtc ccctcaatca cacggattgt actggttaac attctgttgg      120
157 cgacgttggg tttgggagct gcagtccttc cagcagacaa cagaactgtt tgcgggagtc      180
159 aactctgcac atggtggcac gactccggcg agataaacac cgggtactcct gtacaggcag      240
161 gaaacgttcg acaatcccga aagtactctg tccatgtgag cctggcagac cgtaaccaat      300
163 tctacgactc tttcgtatat gaatcgatac ctaggaacgg caatggcaga atttattctc      360
165 ccaccgaccc acctaacagc aatacattga atagtagcat tgacgacggt atatcaatcg      420
167 aaccatctct cggcatcaac atggcttggg cccagttcga atatagacga gatgtcgaca      480
169 ttaagattac tacaatcgat ggctcaatat tggatggccc tttggacatt gttattcggc      540
171 cgacttctgt taagtactca gtcaaaagat gtgtgggtgg tatcattatt agagtcacct      600
173 atgatcccaa tggctgaaaa ttctctgttg agttaagag tgacctttac agttacctct      660
175 ccgacgggtc gcaatatgtg acctctggag ggagcgtggg tgggtgtggg ccaaaaaatg      720
177 ccctggtgat ctttgccagc cctttcttgc cacgggatat ggttcctcat atgacaccac      780
179 acgacaccca gacaatgaag ccgggcccac tcaataatgg ggactggggg tcaaagccta      840
181 tactctactt cccgcctggc gtatactgga tgaacgagga tacctctggg aaccccgga      900
183 agctcggctc aaatcatatg cggctggatc ccaataccta ctgggtccat ctagccccag      960
185 gagcctatgt gaaaggagcc attgagtatt tcacgaagca aaatttctat gcaacgggtc     1020
187 atggcggttct ctcaggtgag aactatgttt atcaggccaa tgcagctgat aactactatg     1080
189 ccgtcaagag tgatggcaca agcttgagaa tgtggtggca caacaacctt ggaggcggtc     1140
191 aaacatggtt ttgcatgggg cccaccatta atgcaccgcc gtttaatacg atggacttca     1200
193 acggaactc taatatttcc agccggatta gtgactataa gcaggttggc gcttattttt     1260
195 tccaaacaga cggaccggag atctacgagg acagtgttgc ccatgacgtc ttctggcatg     1320
197 ttaatgatga tgccatcaag acatattatt ccggagcttc aatttcacga gcaaccatct     1380
199 ggaagtgtca caatgacccg atcatacaga tgggctggac gtcacgaaat ctcaccggaa     1440
201 tcagcattga taacctgcac gtcattccaca cgagatatat caaatctgaa acagtgggtc     1500
203 cttcagcaat cattggagcg tctccattct acgcaagtgg aatgactgtt gatcccagcg     1560
205 agtccatcag catgaccatc tctaactgtg tgtgtgaggg tctatgcccc tcaactgttc     1620
207 gtatcactcc gttcagagc tacaacaacc ttgttgtcaa gaacgtggcc tttcccgatg     1680
209 gactgcagac aaatccaatc ggaataggag agagcattat accagcagct tccggctgta     1740
211 caatggactt ggaaatcaca aactggaccg tcaaaggaca aaaagtcacc atgcaaaact     1800
213 ttcagtcagg gtcacttggc cagttcgata tcgatgggtc atactggggg caatgggtcca     1860
215 taaactaaag ctattcccat tcacctgagt attttcgtgg gttcaatgag ttcttgttac     1920
217 tgatggggcc cttgctagtg gtaaaagtag agggacttgt cctcgccggg cgccaaggaa     1980
219 gttcatgtct tctagttgaa tagtatttgt ttcttctctc tcgttaaaaa aaaaaaaaaa     2040
221 aaaaaaaaaa aa                                     2052
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 18
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:

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230 <223> OTHER INFORMATION: L. starkeyi DX-F primer(sense)  
233 <400> SEQUENCE: 3  
234 gtcccttgag ctcccaac 18  
237 <210> SEQ ID NO: 4  
238 <211> LENGTH: 23  
239 <212> TYPE: DNA  
240 <213> ORGANISM: Artificial Sequence  
242 <220> FEATURE:  
243 <223> OTHER INFORMATION: L. starkeyi DX-R primer(antisense)  
246 <400> SEQUENCE: 4  
247 tcaactagaa ttcatgaact tcc 23

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/588,140

DATE: 08/10/2006

TIME: 10:59:48

Input Set : A:\44352-0010-00-US sequence listing(pct 05 234).txt

Output Set: N:\CRF4\08102006\J588140.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE